
 WISE (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 27 15:57:41 1999: Maspar time 65.43 Seconds

Tabular output not generated. 620.759 Million cell updates/sec

Title: >US-08-956-991-2

Description: (1-1910) from US08956991A.pcp

Perfect Score: 13516

Sequence: 1 MWILALSLRFOSFANFSEDL.....KATGOVTSYICLHLEWTFIC 1910

Scoring table:

PAM 150
 Gap 11

Searched: 170751 seqs, 21265608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part 11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 42.028; Variance 241.419; scale 0.174

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	13516	100.0	1910	32	W42086	Human Down syndrome-c	0.00e-00
2	11110	82.2	1571	32	W42087	Human Down syndrome-c	0.00e-00
3	2081	15.4	455	33	W55045	Neural adhesion molec	8.94e-140
4	740	5.5	1447	26	R68553	Deleted in colorectal	3.28e-41
5	740	5.5	1728	3	R13144	Deleted in Colorectal	3.28e-41
6	631	4.7	1018	16	R87028	Human contactin.	2.11e-33
7	629	4.7	1018	11	R63759	Human contactin (EMBL	2.92e-33
8	623	4.6	1192	32	W57900	Protein of clone C072	7.83e-33
9	606	4.5	1018	22	W06485	Rat contactin ligand	1.27e-31
10	608	4.5	1028	34	W29657	Homo sapiens D185.1	9.15e-32
11	580	4.4	761	16	R92255	Neural cell adhesion	1.74e-30
12	588	4.4	1304	37	W59994	Human neural cell adn	2.41e-30
13	569	4.2	1911	13	R71725	Human PTP-OB.	5.37e-29
14	569	4.2	1911	24	W27225	Human protein tyrosin	5.37e-29
15	549	4.1	582	16	R92256	Neural cell adhesion	1.40e-27
16	525	3.9	1070	20	W08747	Human colon carcinoma	6.89e-26

17	514	3.8	753	39	W83927	Human T85 protein.	4.10e-25
18	486	3.6	1501	14	R72858	Rat receptor type-pro	3.78e-23
19	394	2.9	400	15	R75203	Tyrosine phosphatase	9.24e-17
20	353	2.6	1251	15	R75201	Tyrosine phosphatase	5.88e-12
21	321	2.4	467	17	R84094	NSK2 receptor with pu	8.56e-12
22	319	2.4	467	34	W62575	Alternatively spliced	1.17e-11
23	319	2.4	475	17	R94982	NSK2 extracellular do	1.17e-11
24	322	2.4	478	16	R92718	Mouse muscic-jocalize	7.34e-12
25	322	2.4	478	16	R92716	Mouse muscic-jocalize	7.34e-12
26	319	2.4	863	34	W62569	Mouse muscic-jocalize	1.17e-11
27	319	2.4	867	34	W62583	Mouse receptor tyrosi	1.17e-11
28	322	2.4	868	16	R92717	Mouse muscic-jocalize	7.34e-12
29	320	2.4	868	25	W25610	Rat muscic-specific k	1.00e-11
30	320	2.4	868	25	W25607	Rat Dmk receptor.	1.00e-11
31	326	2.4	869	25	W25506	Human Dmk receptor.	3.95e-12
32	326	2.4	869	25	W25611	Human muscic-specific	3.95e-12
33	319	2.4	871	34	W62568	Mouse receptor tyrosi	1.17e-11
34	319	2.4	871	17	R84087	NSK2 receptor.	1.17e-11
35	319	2.4	873	17	R84092	NSK2 receptor with al	1.17e-11
36	319	2.4	873	34	W52573	Alternatively spliced	1.17e-11
37	319	2.4	881	17	R84091	NSK2 receptor with al	1.17e-11
38	319	2.4	881	34	W62572	Mouse NSK2 (alternati	1.17e-11
39	320	2.4	1225	30	W52289	Homo sapiens cdo tumo	1.00e-11
40	330	2.4	1242	30	W52287	Rattus norvegicus cdo	2.12e-12
41	317	2.3	863	17	R84088	NSK2 receptor with al	1.59e-11
42	302	2.2	1091	27	W41641	Sequence used in dete	1.50e-10
43	264	2.0	1125	30	W52288	Rattus norvegicus cdo	5.22e-08
44	264	2.0	1139	31	W37779	Rattus norvegicus Cla	5.22e-08
45	262	1.9	2327	3	R15468	Human fibronectin.	7.05e-08

ALIGNMENTS

RESULT	1	W42086 standard; Protein: 1910 AA.
ID	W42086;	AC
DT	28-SEP-1998 (first entry)	
DE	Human Down syndrome-cell adhesion molecule DS-CAM1.	
KW	DS-CAM1; Down syndrome-cell adhesion molecule; neural cell;	
KW	signal transduction; trisomy 21; mental retardation;	
KW	holoprosencephaly; corpus callosum agenesis;	
KW	schizophrenia; diagnosis: assay; human.	
OS	Homo sapiens.	
FH	Key	Location/qualifiers
FT	Peptide	1..23
FT	Protein	/label= Sig-peptide
FT		24..1910
FT		/label= Mnt protein
FT	Domain	24..847
FT		/label= ;
FT		/note= "immunoglobulin type-C2 domain"
FT		888..1594
FT	Domain	/label= FBN
FT		1595..1616
FT	Domain	/label= Transmembrane
FT		1617..1910
FT		/label= Cytoplasmic
FT	Domain	24..126
FT		/label= Ig1
FT	Region	127..225
FT		/label= Ig2
FT	Region	226..316
FT		/label= Ig3
FT	Region	317..409
FT		/label= Ig4
FT	Region	410..506
FT		/label= Ig5
FT	Region	507..603
FT		/label= Ig6
FT	Region	604..697
FT		/label= Ig7
FT	Region	698..792

FT /label= 198
FT 793..887
FT /label= 199
FT 46..102
FT Disulfide_bond 145..197
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FT Disulfide_bond 335..385
FT Disulfide_bond 428..484
FT Disulfide_bond 525..575
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FT Disulfide_bond 711..766
FT Disulfide_bond 809..865
FT Disulfide_bond 1307..1359
FT Disulfide_bond 78..80
FT /note= "Asn is N-glycosylated"
FT 106..108
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FT 470..472
FT /note= "Asn is N-glycosylated"
FT 487..489
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FT 658..660
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FT 666..668
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FT 710..712
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FT 748..750
FT /note= "Asn is N-glycosylated"
FT 795..797
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FT 924..926
FT /note= "Asn is N-glycosylated"
FT 1142..1144
FT /note= "Asn is N-glycosylated"
FT 1160..1162
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FT 1250..1252
FT /note= "Asn is N-glycosylated"
FT 1271..1273
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FT 1324..1326
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FT 1341..1343
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FT 1488..1490
FT /note= "Asn is N-glycosylated"
PN W09817795-A1.
PD 30-APR-1998.
PF 23-OCT-1997: U19547.
PR 25-OCT-1996: US-029322.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PI Korenberg JR.
DR N-PSDB: V31981.
PT New isolated Down's Syndrome-cell adhesion molecule - used to
PT development products for detection, diagnosis and therapy of
PT developmental and neurological abnormalities
PS Claim 2: Page 73-78; 109pp; English.
CC This polypeptide comprises Down syndrome-cell adhesion molecule
CC DS-CAM1, a cell surface glycoprotein belonging to a novel subclass
CC of the Ig superfamily with highest homology to neural cell adhesion
CC molecules. Its amino acid sequence was deduced from cDNA clones
CC (see V31981) isolated from a trisomy 21 foetal brain library. A
CC splice variant, DS-CAM2 (see W42087), which is non-membrane bound
CC was also identified. The invention also provides human and murine
CC DS-CAM nucleic acid sequences (see also V31985-88), expression
CC vectors and host cells, transgenic animals, antibodies, antisense
CC oligonucleotides, and primers derived from DS-CAM nucleic acid.
CC DS-CAM polypeptides are associated with developmental and
CC neurological processes. They can be used in e.g. neural prosthetic
CC devices used in entubulation methods of repairing (regenerating)
CC damaged or severed peripheral nerves, and also in bioassays to

CC identify agonists and antagonists. The products can also be
CC used in detection, diagnosis and therapy of developmental and
CC neurological abnormalities such as Down syndrome, mental
CC retardation, holoprosencephaly, agenesis of the corpus callosum,
CC or schizencephaly.
SQ Sequence 1910 AA:

Query Match 100.0%: Score 13516; DB 32; Length 1910;
Best Local Similarity 100.0%: Pred. No. 0.00e+00;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mwlaiaiaifgsianvisedihsalyfnasigevfastgtclvpccaagipvtirwyl 60
Qy 1 mwlaiaiaifgsianvisedihsalyfnasigevfastgtclvpccaagipvtirwyl 60
Db 61 atgeeiaydvpgirihvbnlylqifripssicllindnlyccaaenpskirsqdhika 120
Qy 61 atgeeiaydvpgirihvbnlylqifripssicllindnlyccaaenpskirsqdhika 120
Db 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtslvsgsrflitsta 180
Qy 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtslvsgsrflitsta 180
Db 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtslvsgsrflitsta 180
Qy 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtslvsgsrflitsta 180
Db 181 lyikdvnedglynrcitrlhytgetrgnsarlfvsdpansapsildgfhrkamaq 240
Qy 181 lyikdvnedglynrcitrlhytgetrgnsarlfvsdpansapsildgfhrkamaq 240
Db 241 rvelpckaiaqhppeydwylkdmpltsgrfqtvtgqllienirpsdssyscveenryg 300
Qy 241 rvelpckaiaqhppeydwylkdmpltsgrfqtvtgqllienirpsdssyscveenryg 300
Db 241 rvelpckaiaqhppeydwylkdmpltsgrfqtvtgqllienirpsdssyscveenryg 300
Qy 241 rvelpckaiaqhppeydwylkdmpltsgrfqtvtgqllienirpsdssyscveenryg 300
Db 301 takvigrlyvkkpikatisprkksvsgvsiscvtgtedgelwyvngelimgknv 360
Qy 301 takvigrlyvkkpikatisprkksvsgvsiscvtgtedgelwyvngelimgknv 360
Db 361 ritginhenlimdhmvsdsgayqctvrkdklsaqdyvqvledgtipkllisafsekvsp 420
Qy 361 ritginhenlimdhmvsdsgayqctvrkdklsaqdyvqvledgtipkllisafsekvsp 420
Db 421 aeprvslmcnkvkqcpilpctivclddprikgsnrisgmitsenrvsnynissgyrdg 480
Qy 421 aeprvslmcnkvkqcpilpctivclddprikgsnrisgmitsenrvsnynissgyrdg 480
Db 481 vyrciansagvnylgarivnrgpasirpknltaiagrdtyhcrvipyrysikvwn 540
Qy 481 vyrciansagvnylgarivnrgpasirpknltaiagrdtyhcrvipyrysikvwn 540
Db 541 snllpfhrcqvafemutlksdvqkvedeaylcnvlyvqpqlstsqsvhvtvkypfiq 600
Qy 541 snllpfhrcqvafemutlksdvqkvedeaylcnvlyvqpqlstsqsvhvtvkypfiq 600
Db 601 pfeprfsisggrvllpcvsvsgdplilcltwkdqgrpipslyctianidftssrlsnls 660
Qy 601 pfeprfsisggrvllpcvsvsgdplilcltwkdqgrpipslyctianidftssrlsnls 660
Db 661 lmhngntctiarlnaaavehqsqilivrvpkfvvqprddgfygkavllncsaegpyvt 720
Qy 661 lmhngntctiarlnaaavehqsqilivrvpkfvvqprddgfygkavllncsaegpyvt 720
Db 721 lvmfkskagvpgpqpialnqriovlslngslllkhvveedsgyllkvsndvadvyskm 780
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Db 781 yltvklpamitsynttclatagqgkkmescanabekpiyvwkedtlinpemaarylvsck 840
Qy 781 yltvklpamitsynttclatagqgkkmescanabekpiyvwkedtlinpemaarylvsck 840
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Qy 841 evgeevstqlipvtvredsgfscchainsgygedrglqitvgeppdppeleikvkat 900
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Qy 901 ltlwmgfdgnsptiygdielcknksdswdsagrtkdvspqinsatidihpsstysim 960

WIDEOR (TM)

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Msrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 27 16:17:32 1999; MasPar time 21.88 Seconds
Tabular output not generated. 886.258 Million cell updates/sec

Title: >US-08-956-991-2
Description: (1-1910) from US08956991A.pep
Perfect Score: 13516
Sequence: 1 MWILSLSFOSFANVFSEDL.....KAIGVTSICLHLEMTFC 1910

Scoring table: PAM 150
Gap 11

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCIT9_COMB 4:backfiles1

Statistics: Mean 39.122; Variance 235.804; scale 0.166

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	740	5.5	1447	3	PCT-US94-0 Sequence 2, Applicatio	5.56e-40
2	629	4.7	1018	1	US-08-408- Sequence 6, Applicatio	2.28e-32
3	629	4.7	1018	1	US-08-408- Sequence 6, Applicatio	2.28e-32
4	629	4.7	1018	1	US-08-714- Sequence 6, Applicatio	2.28e-32
5	606	4.5	1018	2	US-08-452- Sequence 2, Applicatio	8.48e-31
6	569	4.2	1911	2	US-08-800- Sequence 2, Applicatio	2.79e-28
7	569	4.2	1911	1	US-08-348- Sequence 5, Applicatio	2.79e-28
8	569	4.2	1911	3	PCT-US94-1 Sequence 5, Applicatio	2.79e-28
9	486	3.6	1501	2	US-08-716- Sequence 3, Applicatio	1.13e-22
10	486	3.6	1501	2	US-08-447- Sequence 3, Applicatio	1.13e-22
11	379	2.8	946	3	PCT-US95-0 Sequence 13, Applicati	1.51e-15
12	322	2.4	478	3	PCT-US95-0 Sequence 15, Applicati	8.04e-12
13	322	2.4	860	3	PCT-US95-0 Sequence 19, Applicati	8.04e-12
14	322	2.4	868	3	PCT-US95-0 Sequence 21, Applicati	8.04e-12
15	320	2.4	868	1	US-08-374- Sequence 1, Applicatio	1.08e-11
16	320	2.4	868	2	US-08-644- Sequence 1, Applicatio	1.08e-11
17	326	2.4	869	1	US-08-374- Sequence 16, Applicati	4.43e-12
18	326	2.4	869	2	US-08-644- Sequence 29, Applicati	4.43e-12
19	282	2.1	2231	2	US-08-153- Sequence 16, Applicati	3.01e-09
20	262	1.9	2324	3	PCT-US95-0 Sequence 1, Applicatio	5.59e-08
21	262	1.9	2324	4	US-08-283- Sequence 1, Applicatio	5.59e-08
22	262	1.9	2327	4	5455158-1 Patent No. 5455158	5.59e-08
23	262	1.9	2446	2	US-08-551- Sequence 2, Applicatio	5.59e-08

24	262	1.9	2446	3	PCT-US93-1	Sequence 2, Applicatio	5.59e-08
25	233	1.7	252	2	US-08-414-	Sequence 57, Applicati	3.67e-06
26	227	1.7	252	2	US-08-414-	Sequence 56, Applicati	8.65e-06
27	235	1.7	287	2	US-08-414-	Sequence 49, Applicati	2.76e-05
28	239	1.7	287	2	US-08-414-	Sequence 48, Applicati	6.50e-05
29	239	1.7	304	2	US-08-414-	Sequence 44, Applicati	6.50e-05
30	229	1.7	308	2	US-08-414-	Sequence 46, Applicati	6.50e-05
31	235	1.7	310	2	US-08-414-	Sequence 45, Applicati	2.76e-05
32	235	1.7	315	2	US-08-414-	Sequence 47, Applicati	2.76e-05
33	229	1.7	325	2	US-08-414-	Sequence 42, Applicati	6.50e-05
34	229	1.7	325	2	US-08-414-	Sequence 41, Applicati	6.50e-05
35	235	1.7	338	2	US-08-414-	Sequence 43, Applicati	2.76e-05
36	235	1.7	338	2	US-08-414-	Sequence 43, Applicati	2.76e-05
37	234	1.7	419	4	US-08-835-2	Patent No. 5169835.	3.18e-06
38	232	1.7	549	2	US-08-836-	Sequence 11, Applicati	4.24e-06
39	232	1.7	574	2	US-08-836-	Sequence 21, Applicati	4.24e-06
40	227	1.7	642	1	US-08-217-	Sequence 17, Applicati	8.65e-05
41	227	1.7	734	2	US-08-389-	Sequence 17, Applicati	8.65e-05
42	234	1.7	828	1	US-08-261-	Sequence 2, Applicatio	3.18e-05
43	222	1.6	338	2	US-08-414-	Sequence 60, Applicati	1.76e-05
44	223	1.6	424	4	US-08-835-6	Patent No. 5169835.	1.53e-05
45	219	1.6	999	1	US-08-252-	Sequence 2, Applicatio	2.69e-05

ALIGNMENTS:

RESULT	1	STANDARD:	PRT:	1447 AA.
ID	PCT-US94-05277-2			
XX	xxxxxx			
AC				
DT				
DE	Sequence 2, Application PC/TUS9405277			
XX				
CC	Sequence 2, Application PC/TUS9405277			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Bruskin, Arthur			
CC	APPLICANT: Jarosz, David E.			
CC	APPLICANT: Johnson, Karen			
CC	APPLICANT: Kinzel, Kenneth W.			
CC	APPLICANT: Vogelst. in, Bert			
CC	APPLICANT: Zabrecky, James R.			
CC	TITLE OF INVENTION: Antibodies Specific for DCC Gene Product			
CC	NUMBER OF SEQUENCES: 2			
CC	CORRESPONDENCE ADDRESSES:			
CC	ADDRESS: Banner, Birch, McKie & Beckett			
CC	STREET: 1001 G Street, N.W.			
CC	CITY: Washington			
CC	STATE: D.C.			
CC	COUNTRY: USA			
CC	ZIP: 20001			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Patentin Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: PCT/US94/05277			
CC	FILING DATE:			
CC	CLASSIFICATION:			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Kagan, Sarah A.			
CC	REGISTRATION NUMBER: 32,141			
CC	REFERENCE/DOCKET NUMBER: 01107.42709			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: 202.508.9100			
CC	TELEFAX: 202.508.9299			
CC	TELEX: 197430 BBMB UT			
CC	INFORMATION FOR SEQ ID NO: 2:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 1447 amino acids			
CC	TYPE: amino acid			

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MIRCH_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 27 16:03:06 1999; MasPar time 75.66 Seconds
1011.559 Million cell updates/sec
Tabular output not generated.

Title: >US-08-956-991-2
Description: (1-1910) from US08956991A.pap
Perfect Score: 13516
Sequence: 1 MWILALSLFOSFANWFSED.....KALGOVTSYICLHLEMTFC 1910

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: p1r60
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 57.625; Variance 121.630; scale 0.474

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	809	5.0	1028	2	I58164	BIG-1 protein - rat	3.78e-121
2	786	5.8	1028	2	A53449	plasmacytoma-associat	9.58e-117
3	740	5.5	1447	2	A54100	tumor suppressor prot	5.75e-108
4	744	5.5	7962	2	I18346	elastic tctin - human	9.95e-109
5	720	5.3	1040	2	A49356	transient axonal glyco	3.65e-104
6	703	5.2	1036	2	S22383	axonal precursor - Af	6.14e-101
7	701	5.2	1040	2	A34595	axonal glycoprotein T	1.47e-100
8	707	5.2	1427	2	I51669	tumor suppressor - Af	1.07e-101
9	680	5.0	1239	2	A43425	Bravo/Nr-CAM cell adh	1.39e-95
10	677	5.0	1268	2	A39640	neural cell adhesion	5.12e-96
11	663	4.9	1010	2	JU0094	F11 protein precursor	2.25e-93
12	663	4.9	1091	2	S01998	contactin precursor -	2.36e-87
13	631	4.7	1018	2	A54744	contactin 1 precursor	5.60e-87
14	629	4.7	1018	2	I37246	contactin - human	2.36e-87
15	631	4.7	1020	2	S05944	neural cell surface	2.36e-87
16	631	4.7	1021	2	A57112	contactin precursor -	1.76e-88
17	637	4.7	1259	2	S36126	neural cell adhesion	1.76e-88
18	637	4.7	1260	2	S05479	neural cell adhesion	4.81e-89
19	640	4.7	1898	2	S46216	leukocyte antigen-rel	2.73e-85
20	620	4.6	1257	2	A41060	neural cell adhesion	1.15e-85
21	622	4.6	1894	2	C54689	protein-tyrosine-phos	5.59e-84
22	613	4.5	1018	2	JC4211	neural adhesion prote	3.13e-83
23	609	4.5	2029	1	TDFLTK	protein-tyrosine-phos	3.13e-83

RESULT ENTRY	1	ALIGNMENTS
TITLE	I58164	#type complete
ORGANISM	BIG-1 protein - rat	
DATE	26-Jul-1996	#formal_name Rattus norvegicus #common_name Norway rat
ACCESSION	I58164	26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 18-Sep-1998
REFERENCE	I58164	
authors	Yoshihara, Y., Kawasaki, M., Tanai, A., Tamada, A., Nagata, S., Kagamiyama, H., Morii, K.	
#journal	Neuron (1994) 13:415-426	
#title	BIG-1: a new TAG-1/F3-related member of the immunoglobulin superfamily with neurite outgrowth-promoting activity.	
#cross-references	MUID:94338697	
#accession	I58164	
##status	preliminary: translated from GR/EMBL/DBJ	
##molecule_type	mRNA	
##residues	1-1028	#label RES
##cross-references	EMBL:U11031; NID:9563132; PID:9563133	
GENETICS		
#gene	BIG-1	
CLASSIFICATION	#superfamily contactin; fibronectin type III repeat homology; Immunoglobulin homology	
SUMMARY	#length 1028 #molecular_weight 112788 #checksum 5866	
Query Match	6.0%; Score 809; DB 2; Length 1028;	
Best Local Similarity	24.7%; Pred. No. 3.78e-121;	
Matches	250; Conservative 249; Mismatches 447; Indels 66; Gaps 54;	

Db	25	GPVFKPEP-SNSIPP-V-GSEDKITLNCARNPSPDHRRMQLNGSDITSLDHRK-L 79
Oy	306	GRLYKQPLKATISPRKYSQVSLSCTGTEDQELSWYNGILLNGKRVRTIGI 365
Db	80	NGNLIVINPRNMDTGSVOCEFA-TNSLGTIVSREAKLOFAYLENFRSRMSRVAREQ 138
Oy	366	NHENTIMDHMKV-DGAVYQCFVRKDKLSADQYOVVLEDC-TRKIISAPSEK-VSPA 422
Db	139	GVLLCGPPPHSGELSLVAVNEPSEFVEDSRFRVSOETGHLYIAVPESDGVN7TCV 198
Oy	423	PSLMCNKVG-TPLPTIMWTLDDP-ILKGSRR-ISO---M-ITS-E-GNVSYLNIS 472
Db	199	TSTVTNARYLSPPLVLRSDGVMGEYEPKIELOPETLPAPAKG-STV-K--LECFAL 252
Oy	473	SSQVDDGVY-RCTA-N-NSAGVY-LYQARINVRPASIRPKNITAIAGDITIHQV 528
Db	253	GNVPQJNMV-RRSDGMPPTK-IKLRFNGVLEIPNFQOE-DTSYEC-IAENSRGNVA 308

QY 529 GYPYYSIKWYKNSNLLPFRHROVAFEN-NGTLKLSDVOKVEDEGEYTCNVLVQPOLSTSQ 587

Db 309 RGRLLTYVANKPYWOLLKDVETAVEDSLYWECPRA-SGKPKPSTRMLKNGAL--VLEERIQ 365

QY 588 SVHATYVAKVPPF-IQPFEPFRFSIGORVFIQPCVAVSGDLPIITITWQDGRPIGSGLVITID 646

Db 366 -IE-NGALTIANLVNDSGFCOIAENKHGLIYSSAELVLVASAPFSNPKMKMIOVOV 423

QY 647 NIDFTSSLRIISNLHNGNYTCIARNEAAVEHOSOL-IVRPPKFFVQV-P-RDODGI-Y 703

Db 424 GSVLIIDCKKSPRALSEFK--KGDYVVR-EQ-A--RISLNDGGLKIMNYTKADGI 476

QY 704 GKAVIILNCSGEGIPVPIYWKFSKGAGVPOFQIALNGRIQVLSNGLIKHVEEDSGY 763

Db 477 YTCIAENQFGKANGTTO-LVYTEPTRIILAPSNMDVAVGESIILPCOVQHDPLDIMFAM 535

QY 764 YLCKVSNVDGADYSKMYLTVKIPAMITSYPNITLATQOQKREMSCTAJGEXPI-IV-RW 821

Db 536 YFNGTLLDFKKDGSHEF-K-VGSSSGDLMIRNIQLKHSKGYVCNVOFGVDSVSAELI 593

QY 822 EKEDRIINPEMARIYVSTKEVGEVISTLOILPTVREDSGFESCHAINSDEGRGIIQLT 881

Db 594 VRSGPPEVNVKVEITDITAOIWSMTGIDSHSPVISYAVQARTPFSGVQWNYRTVPEAI 653

QY 882 VOEPDPPPE-IEIKDYKAKRTIILRWTFGFGNSPIITGYDILCKNK-SDSWSAQRTKD-V 538

Db 654 DCKTRTATVELNPMWYEFRRVYVASKIGGEPSSLSEKRTTEAPAEVAPSPVSGGGS 713

QY 939 SPOLNSATIIDIHPSSTYSIRMYAKNRIGSEPS-NELTITADEAPADGPOQVHLEPIS 997

Db 714 RSELVITMDPVEELONGGFGFYVAFRPLGVTTWIO-TVVT-SPDNPRYFRNESTIVPF 771

QY 998 SOSIRVYWKAPKHHLONGIIRGOIGREYSTGNGFQFNISVDTSGDSVYITLDNLNF 1057

Db 772 SPYEVKGVYNNKGEPSPVTVTFSAEERTVAPSHISHSLSSEIEVSNMTITWKS 831

QY 1058 TOYGLVQACNRAGTGPSOELIITITLEDVPSYPPEVQAIATSPESISISWSTLKEAL 1117

Db 832 NGRLIGEVRRVWNGGEESSSKYKAVAGNOTSAVLRLGKSNLAYVTVARVYNTAGAPFS 891

QY 1118 NGILOGFRVITYWANLMDGELGEIKNITTTQPSLELDGLEYKTNYSIOVLAFTRAGDGVRS 1177

Db 892 ATVNATTKTPPSOPPGNVVWNAITDTVLLNMEQVKALENSEVYGVYFRTSSQNNVO 951

QY 1178 EOIFRTKEDVGPAGVKAASAMVFSW--LPPLKINGIIRKTYVFCSHPTVIS 1235

Db 952 VLNTNKTSAELLP-I-KE-DYIIEVKAITDGGDGTSSGOIIRIPRITSMAR 1000

QY 1236 EFASPDSPFSYRIPNLSRNROYSVWVAVTISAGRNSSEIITVEPLAKAPAR 1287

RESULT 2

ENTRY A53449 #type complete

TITLE plasma cytoma-associated neuronal glycoprotein PANG - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 25-Aug-1999 #sequence_revision 25-Aug-1995 #text_change 18-Sep-1998

ACCESSIONS A53449

REFERENCE A53449

AUTHORS Connelly, M.A.; Grady, R.C.; Mushinski, J.F.; Marcu, K.B.

JOURNAL P. C. Natl. Acad. Sci. U.S.A. (1994) 91: 137-1341

TITLE PANG, a gene encoding a neuronal glycoprotein, is ectopically activated by intracisternal A-type particle long terminal repeats in murine plasmacytomas.

#cross-references MUID:94151325

#accession A53449

#status preliminary

#molecule_type mRNA

#residues 1-1028 ##label CON

#cross-references GB:101991; NID:q200056; PID:q200057

CLASSIFICATION #superfamily contactin; fibronectin type III repeat homology; immunoglobulin homology

KEYWORDS glycoprotein

SUMMARY

#length 1028 #molecular-weight 113151 #checksum 4174

Query Match 5.88; Score 786; DB 2; Length 1028;

Best Local Similarity 24.68; Pred. No. 9,58e-117;

Matches 249; Conservative 246; Mismatches 451; Indels 65; Gaps 54;

Db 25 GPVFIKEP-SNSIPP--VDSE-DKILITLNCFARGNSPHYRMOLNGSDIDTSLDHRK-L 79

QY 306 GRLLVQKPLKATISIPRKVKSVSQVSLSCSYGTGEOELSWRNELINPGKNVIRITGI 365

Db 80 NGNLIIVNPNRNDGTSYOCFA-TNSLGTIVSREAKLOFAYLENFKTRMRRTVSVRQ 138

QY 366 NHEMLIDHWKS-DGAYOCFAKDKLSADYVQVLEDEG-TPKIISAFSEKV-VSPA 422

Db 139 GVVLICGPPRHSGLSYAWYFNEPSPFVEEDSRILYSQETGHIYIAKVEPSDVGNVCV 198

QY 423 PVLMLCNVKG-TPLPTITWITLDDP-ILKKGSH-ISO---M-ITS-E-GNVSITLNTS 472

Db 199 TSTVNTFRVLGSPITPLVLRSDGVGEYEPKIEVOFPETLPAKG-STV-R--LECFAL 252

QY 473 SSOYRBDGVY-RCTA-N-NSAGV-LVQARINVRGPASTIRPMKNITFAIAGRTYIHCRVI 528

Db 253 GNPVPOIWM-RRSDGMPPNK-ILKRFNGMLEIQNFQOE-DTGSYE-GIAENSRKKNVA 308

QY 529 GYPYYSIKWYKNSNLLPFRHROVAFEN-NGTLKLSDVOKVEDEGEYTCNVLVQPOLSTSQ 587

Db 309 RGRLLTYVANKPYWOLLKDVETAVEDSLYWECPRA-SGKPKPSTRMLKNGAL--VLEERIQ 365

QY 588 SVHATYVAKVPPF-IQPFEPFRFSIGORVFIQPCVAVSGDLPIITITWQDGRPIGSGLVITID 646

Db 594 VRSGPPEVNVKVEITDITAOIWSMTGIDSHSPVISYAVQARTPFSGVQWNYRTVPEAI 653

QY 882 VOEPDPPPE-IEIKDYKAKRTIILRWTFGFGNSPIITGYDILCKNK-SDSWSAQRTKD-V 538

Db 654 DCKTRTATVELNPMWYEFRRVYVASKIGGEPSSLSEKRTTEAPAEVAPSPVSGGGS 713

QY 939 SPOLNSATIIDIHPSSTYSIRMYAKNRIGSEPS-NELTITADEAPADGPOQVHLEPIS 997

Db 714 RSELVITMDPVEELONGGFGFYVAFRPLGVTTWIO-TVVT-SPDNPRYFRNESTIVPF 771

QY 998 SOSIRVYWKAPKHHLONGIIRGOIGREYSTGNGFQFNISVDTSGDSVYITLDNLNF 1057

Db 772 SPYEVKGVYNNKGEPSPVTVTFSAEERTVAPSHISHSLSSEIEVSNMTITWKS 831

QY 1058 TOYGLVQACNRAGTGPSOELIITITLEDVPSYPPEVQAIATSPESISISWSTLKEAL 1117

Db 832 NGRLIGEVRRVWNGGEESSSKYKAVAGNOTSAVLRLGKSNLAYVTVARVYNTAGAPFS 891

QY 1118 NGILOGFRVITYWANLMDGELGEIKNITTTQPSLELDGLEYKTNYSIOVLAFTRAGDGVRS 1177

Db 892 ATVNATTKTPPSOPPGNVVWNAITDTVLLNMEQVKALENSEVYGVYFRTSSQNNVO 951

QY 1178 EOIFRTKEDVGPAGVKAASAMVFSW--LPPLKINGIIRKTYVFCSHPTVIS 1235

Db 952 VLNTNKTSAELLP-I-KE-DYIIEVKAITDGGDGTSSGOIIRIPRITSMAR 1000

QY 1236 EFASPDSPFSYRIPNLSRNROYSVWVAVTISAGRNSSEIITVEPLAKAPAR 1287

 WIRE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jul 27 16:07:31 1999: Maspar time 52.29 Seconds
 1032.554 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-956-991-2
 Description: (1-1910) from US08956991A.pep
 Perfect Score: 13.15
 Sequence: 1 MMLALSLPQSFANFSEDL.....KAIGVTSYICLTLEWTFC 1910

Scoring table: PAM 150
 Gap 11
 Searched: 77977 seqs, 28268293 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 58.685: Variance 101.910: scale 0.576

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	744	5.5	1447	1	DCC_MOUSE	3.51e-132
2	740	5.5	1447	1	DCC_HUMAN	2.94e-131
3	720	5.3	1040	1	AXOI_HUMAN	1.21e-126
4	703	5.2	1036	1	AXOI_CHICK	9.86e-123
5	701	5.2	1040	1	AXOI_RAT	2.84e-122
6	677	5.0	1284	1	NRCA_CHICK	9.14e-113
7	663	4.9	1010	1	CONT_CHICK	1.46e-113
8	631	4.7	1018	1	CONT_HUMAN	2.92e-106
9	631	4.7	1020	1	CONT_MOUSE	1.26e-107
10	637	4.7	1259	1	CAML_RAT	1.26e-107
11	637	4.7	1260	1	CAML_MOUSE	9.27e-104
12	620	4.6	1257	1	CAML_HUMAN	2.91e-101
13	609	4.5	2029	1	LAR_DROME	9.03e-99
14	598	4.4	1887	1	PTPF_HUMAN	1.90e-92
15	570	4.2	837	1	NCM2_MOUSE	1.20e-90
16	562	4.2	837	1	NCM2_HUMAN	1.20e-90
17	562	4.2	1239	1	NRG_DROME	2.38e-93
18	574	4.2	1912	1	PTPD_HUMAN	2.38e-93
19	558	4.1	1091	1	NCAL_CHICK	9.48e-85
20	543	4.0	848	1	NCAL_HUMAN	2.19e-85
21	524	3.9	1088	1	NCAL_XENTLA	3.87e-82
22	523	3.9	1092	1	NCAL_XENTLA	6.46e-82
23	531	3.9	1266	1	NGCA_CHICK	1.06e-83

24	509	3.8	761	1	NCAL_HUMAN	8.45e-79
25	498	3.7	853	1	NCAL_BOVIN	2.33e-76
26	496	3.7	1115	1	NCAL_MOUSE	6.47e-76
27	492	3.6	858	1	NCAL_RAT	4.97e-75
28	478	3.5	725	1	NCAL_MOUSE	6.14e-72
29	401	3.0	868	1	PAS2_SCHAM	3.59e-55
30	402	3.0	3707	1	PGBM_MOUSE	2.19e-55
31	378	2.8	811	1	FS22_DROME	2.95e-50
32	378	2.8	873	1	FS21_DROME	2.95e-50
33	364	2.7	4393	1	PGBL_HUMAN	2.73e-47
34	313	2.3	2477	1	FINC_RAT	1.13e-36
35	308	2.3	2477	1	FINC_MOUSE	1.13e-36
36	313	2.3	2481	1	UN52_CAEAL	1.13e-36
37	294	2.2	2265	1	FINC_BOVIN	8.32e-33
38	287	2.1	345	1	OPCM_BOVIN	2.14e-31
39	284	2.1	345	1	OPCM_HUMAN	8.55e-31
40	279	2.1	345	1	OPCM_RAT	8.54e-30
41	286	2.1	1131	1	CPSE_CHICK	3.40e-31
42	262	1.9	333	1	AMAL_DROME	1.97e-26
43	255	1.9	353	1	CEPU_CHICK	4.60e-25
44	257	1.9	1328	1	FINC_PLEMA	1.87e-25
45	262	1.9	2386	1	FINC_HUMAN	1.97e-26

ALIGNMENTS

RESULT 1
 ID DCC_MOUSE STANDARD: PRT: 1447 AA.

AC P70211;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.

NC MUS MUSCULUS (MOUSE)
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.

RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE; 96112625.

RA COOPER H.M., ARMES P., BRITTO J., GAD J., WILKS A.F.;
 RT Cloning of the mouse homologue of the deleted in colorectal cancer gene (mdcc) and its expression in the developing mouse embryo.";

RL ONCOGENE 11:2243-2254(1995).
 RN [2]

RP REVISIONS.

RC STRAIN-BALB/C; TISSUE-BRAIN;
 RA COOPER H.M.;

RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/UDJ DATA BANKS.
 CC -1- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE

CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
 CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.

CC -1- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
 CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION

CC AND REMAIN AT THIS LEVEL IN THE ADULT.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM

CC THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD
 CC FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY

CC ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

CC 4 C2-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.

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MSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run On: Tue Jul 27 16:11:31 1999; Maspar time 107.09 Seconds

Tabular output not generated. 973.465 Million cell updates/sec

Title: >US-08-956-991-2

Description: (1-1910) from US08956991A.pep

Perfect Score: 13516

Sequence: 1 MMLALSLFQSFANVFSEDL.....I IGVVSYICLHLEKTCFC 1910

Scoring table: PAM 150

Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl9
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 56.959; Variance 104.912; scale 0.543

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	ID	Description	Pred. No.
1	13406	99.2	886	4	060468 DOWN SYNDROME CELL ADH	0.00e+00
2	11119	82.3	1571	4	060469 DOWN SYNDROME CELL ADH	0.00e+00
3	809	6.0	1028	11	062682 BIG-1 PROTEIN PRECURSO	1.99e-139
4	785	5.8	1028	11	007409 PLASMACYTOMA-ASSOCIATE	2.23e-134
5	741	5.5	1445	11	063155 COLORECTAL TUMOR SUPP	1.57e-124
6	744	5.5	7962	4	010465 TITIN, SKELETAL MUSCLE	3.47e-125
7	734	5.4	1099	11	P97527 NB-2.	5.28e-123
8	707	5.2	1427	13	091562 TUMOR SUPPRESSOR.	4.01e-117
9	695	5.1	1026	11	062845 NEURAL CELL ADHESION P	1.62e-114
10	689	5.1	1277	13	098902 NEURAL CELL ADHESION M	3.26e-113
11	696	5.1	1377	11	P97603 NEOGENIN (FRAGMENT).	9.86e-115
12	694	5.1	1395	5	044824 ROUNDABOUT 1.	2.68e-114
13	692	5.1	4162	13	098818 CONNECTIN/TITIN (FRAGM	7.28e-114
14	674	5.0	1224	4	000533 NEURAL CELL ADHESION M	5.82e-110
15	667	4.9	1005	13	P79921 CONTRACTIN/F3/FT11.	1.91e-108
16	668	4.9	1009	13	093250 CONTRACTIN A.	1.16e-104
17	647	4.8	1612	11	089026 DUT11 PROTEIN.	3.99e-104
18	644	4.8	5198	5	075518 HEMICENTIN PRECURSOR.	1.77e-103
19	630	4.7	1021	11	063198 RAT NEURAL ADHESION MO	1.84e-100
20	638	4.7	1461	4	000340 NEOGENIN.	3.48e-102

21	634	4.7	1461	4	092859 NEOGENIN.	2.53e-101
22	629	4.7	1651	11	055005 TRANSMEMBRANE RECEPTOR	3.02e-100
23	640	4.7	1898	11	064604 LEUKOCYTE COMMON ANTIG	1.29e-102
24	627	4.6	1180	4	015051 KIAA0343.	8.14e-100
25	617	4.6	1197	13	090478 ADHESION MOLECULE L1.1	1.15e-97
26	620	4.6	5197	5	010036 HYPOTHETICAL 571.5 KD	2.60e-98
27	613	4.5	1018	6	028106 F3/FT11/CONTRACTIN PREC	8.30e-97
28	612	4.5	1264	5	P91767 NEUROGLIAN.	1.36e-96
29	583	4.4	1028	11	P97528 NB-3.	1.88e-91
30	588	4.4	1299	4	015179 NCAM PROTEIN.	1.88e-91
31	578	4.3	1209	11	P70232 CLOSE HOMOLOGUE OF L1	2.57e-89
32	580	4.3	1277	13	090284 L1-LIKE CELL ADHESION	9.62e-90
33	587	4.3	1323	13	008476 CONNECTIN (TITIN) (FRA	3.08e-91
34	567	4.2	1215	11	P97685 NG-CAM RELATED CELL AD	5.65e-87
35	566	4.2	1904	11	064699 PROTEIN TYROSINE PHOSP	9.29e-87
36	570	4.2	1907	11	064503 PROTEIN TYROSINE PHOSP	1.31e-87
37	568	4.2	1911	1	015718 PTPSIGMA PRECURSOR (EC	3.48e-87
38	550	4.1	1239	5	061541 NEUROGLIAN.	2.34e-83
39	550	4.1	1302	5	061542 NEUROGLIAN.	2.34e-83
40	539	4.0	846	13	057577 NCAM-140.	5.03e-81
41	539	4.0	1100	13	057576 NCAM-180.	5.03e-81
42	545	4.0	1453	11	P97798 NEOGENIN (NEOGENIN PRO	2.69e-82
43	527	3.9	1070	4	013417 TRANSMEMBRANE RECEPTOR	1.74e-78
44	532	3.9	1299	4	092823 HERANO/NR-CAM PRECURSO	1.52e-79
45	530	3.9	1415	5	094155 UNC-40 (11984.6 PROTEI	4.03e-79

ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	1896 AA.
AC	060468				
DT	01-AUG-1998 (TREMBLREL. 07, CREATED)				
DT	01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)				
DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)				
DE	DOWN SYNDROME CELL ADHESION MOLECULE (FRAGMENT).				
GN	DSICAM.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;				
OC	CATARRHINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN.				
RA	YAMAKAWA K., HUO Y.-K., HAENDEL M.A., HUBERT R., CHEN X.-N.,				
RA	LYONS G.E., KORENBERG J.R.;				
RL	SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
DR	EMBL: AF023449; G3169766; ..				
FT	NON_TER	1	1		
SO	SEQUENCE	1896 AA;	209745 MW;	ODE6UCCE CRC32;	
Query Match					
Best Local Similarity 100.0%; P-Val. No. 0.00e+00;					
Matches 1896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Db	1	VFESDLSLFFVNASLOEVFASTTGLVPCPACGIPVTLKMYLATGEIYDVGIRH 60			
Qy	15	VFESDLSLFFVNASLOEVFASTTGLVPCPACGIPVTLKMYLATGEIYDVGIRH 74			
Db	61	VHPGTLQIFPPSPSTLTHDNTTYCTAENPSGKIRSDVHKAVALREPTVAREDOK 120			
Qy	75	VHPGTLQIFPPSPSTLTHDNTTYCTAENPSGKIRSDVHKAVALREPTVAREDOK 134			
Db	121	TMRGVAVAFKCIIPSSVEAYITVSMKEDVSLVSGSRFLITSGALYIKDVONEDGLYN 180			
Qy	135	TMRGVAVAFKCIIPSSVEAYITVSMKEDVSLVSGSRFLITSGALYIKDVONEDGLYN 194			
Db	181	YRCITRRHYTGETQSSARLPVSDPANASPSILDGDRKKAAGQVVELPCALGHPER 240			
Qy	195	YRCITRRHYTGETQSSARLPVSDPANASPSILDGDRKKAAGQVVELPCALGHPER 254			
Db	241	DYRLKDNMPLELSGRQKTYTGLIENIRPSDGSYVCEVSNRGTAKYIGRLYVQPL 300			
Qy	255	DYRLKDNMPLELSGRQKTYTGLIENIRPSDGSYVCEVSNRGTAKYIGRLYVQPL 314			

